

10664423-3vsscn1a_rat.txt

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 5, 2008, 12:26:52 ; Search time 1 Seconds
(without alignments)
4.036 Million cell updates/sec

Title: us-10-664-423a-3
Perfect score: 10403
Sequence: 1 MEQTVLVPPCPDSFNFFTRE. TKPI VEKHEQEGKDEKAKGK 2009

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 2009 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: scn1a_rat.uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY					
Result No.	Score	Query Match	Length	DB ID	Description
1	10258	98.6	2009	1 SCN1A_RAT	Sodium channel protein

ALIGNMENTS

RESULT 1

SCN1A_RAT

ID SCN1A_RAT STANDARD; PRT; 2009 AA.
AC P04774;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 27-JUN-2006, entry version 67.
DE Sodium channel protein type 1 subunit alpha (Sodium channel protein type 1 subunit alpha) (Voltage-gated sodium channel subunit alpha Nav1.1) (Sodium channel protein, brain 1 subunit alpha).
GN Name=Scn1a;
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchoptognathires; Gires; Rodentia; Sciurognathhi;
CC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RP NUCLEOTI DE SEQUENCE [mRNA].
RX MEDLI NE=86146901; PubMed=3754035; DOI=10.1038/320188a0;
RA Noda M, Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M,
RA Takahashi H., Numa S.;
RT "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL Nature 320: 188-192(1986).
RN [2]
RP NUCLEOTI DE SEQUENCE [mRNA].
RX MEDLI NE=87311395; PubMed=2442385;
RA Noda M, Numa S.;
RT "Structure and function of sodium channel.";
RL J. Recept. Res. 7: 467-497(1987).
RN [3]
RP NUCLEOTI DE SEQUENCE [mRNA] OF 177-253.
RC STRAIN=Sprague-Dawley; ISSUE=Brain;
RX MEDLI NE=92051314; PubMed=1658739;
RA Sarao R., Gupta S.K., Auld V.J., Dunn R.J.;
RT "Developmentally regulated alternative RNA splicing of rat brain sodium channel mRNAs.";
RL Nucl. Acids Res. 19: 5673-5679(1991).
CC -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
CC -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
CC -!- SIMILARITY: Belongs to the sodium channel family.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC Copyrighted by the UniProt Consortium see <http://www.uniprot.org/terms>
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DR EMBL; X03638; CAA27286.1; -; mRNA.
DR EMBL; M22253; AAA79965.1; -; mRNA.
DR PIR; A25019; A25019.
DR UniGene; Rh_32079; -.
DR HSSP; P04775; 1BYY.
DR RGD; 69364; Scn1a.
DR GO; GO:0005248; F: voltage-gated sodium channel activity; TAS.
DR GO; GO:0019228; P: generation of action potential; TAS.
DR InterPro; IPR001682; Ca_Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR011992; EF_Hand_type.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_CaM_bd_region.
DR InterPro; IPR005820; M_channel_nl.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008051; Na_channel_1.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PINTS; PR00170; NACHANNEL.
DR PINTS; PR01664; NACHANNEL1.
DR PROSITE; PS50096; IQ_FALSE_NEG.
KW Glycoprotein; Ion transport; Ionic channel; Membrane; Repeat; Sodium

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KW Sod i um channel ; Sod i um t ransport ; T ransmemb rane; T ransport ;
 KW Vol t age- gat ed channel .
 FT CHAI N 1 2009 Sod i um channel pr otein t ype 1 subunit
 al pha.
 / FTI d=PRO_0000048490.
 FT TRANSMEM 124 147 S1 of r epeat || .
 FT TRANSMEM 156 175 S2 of r epeat || .
 FT TRANSMEM 189 207 S3 of r epeat || .
 FT TRANSMEM 214 233 S4 of r epeat || .
 FT TRANSMEM 250 273 S5 of r epeat || .
 FT TRANSMEM 400 425 S6 of r epeat || .
 FT TRANSMEM 763 787 S1 of r epeat || | .
 FT TRANSMEM 799 822 S2 of r epeat || | .
 FT TRANSMEM 831 850 S3 of r epeat || | .
 FT TRANSMEM 857 876 S4 of r epeat || | .
 FT TRANSMEM 893 913 S5 of r epeat || | .
 FT TRANSMEM 967 992 S6 of r epeat || | .
 FT TRANSMEM 1214 1237 S1 of r epeat || | | .
 FT TRANSMEM 1251 1276 S2 of r epeat || | | .
 FT TRANSMEM 1283 1304 S3 of r epeat || | | .
 FT TRANSMEM 1309 1330 S4 of r epeat || | | .
 FT TRANSMEM 1350 1377 S5 of r epeat || | | .
 FT TRANSMEM 1457 1483 S6 of r epeat || | | .
 FT TRANSMEM 1537 1560 S1 of r epeat | V .
 FT TRANSMEM 1572 1595 S2 of r epeat | V .
 FT TRANSMEM 1602 1625 S3 of r epeat | V .
 FT TRANSMEM 1636 1657 S4 of r epeat | V .
 FT TRANSMEM 1673 1695 S5 of r epeat | V .
 FT TRANSMEM 1762 1786 S6 of r epeat | V .
 FT REPEAT 110 454 | .
 FT REPEAT 750 1022 | | .
 FT REPEAT 1200 1514 | | | .
 FT REPEAT 1523 1821 | V .
 FT CARBOHYD 211 211 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 284 284 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 295 295 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 301 301 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 306 306 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 338 338 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 601 601 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 621 621 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 681 681 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 892 892 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1060 1060 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1064 1064 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1080 1080 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1146 1146 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1378 1378 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1392 1392 N- l inked (G cNAc. . .) (Pot ent i al) .
 FT CARBOHYD 1403 1403 N- l inked (G cNAc. . .) (Pot ent i al) .
 SQ SEQUENCE 2009 AA; 228770 MW 6808466F6368373B CRC64;

Quer y Match 98. 6% Score 10258; DB 1; Length 2009;
 Best Local Si milarity 98. 2% Pred. No. 0;
 Mat ches 1972; Conserv ative 24; M smatches 13; Indel s 0; Gaps 0;

Qy 1 MEQTVL VPPGPDSFNFFTRESLAAI ERRI AEEKAKNPKPDKDDDENGPKPNSDLEAGKN 60
 Db 1 MEQTVL VPPGPDSFNFFTRESLAAI ERRI AEEKAKNPKPDKDDDENGPKPNSDLEAGKN 60
 Qy 61 LPFI YGDI PPEMSEPLEDLD PYYI NKKTFI VL NKGKAI FRFSATSALYI LTPFNPLRKI 120
 Db 61 LPFI YGDI PPEMSEPLEDLD PYYI NKKTFI VL NKGKAI FRFSATSALYI LTPFNPLRKI 120

10664423- 3vsscn1a_r at . t xt

Qy	121	AI KI LVHSLFSMLI MCTI LTNCVFMTMSNPPDWTKNVEYFTGI YTFESLI KI I ARGFCL	180
Db	121	AI KI LVHSLFSMLI MCTI LTNCVFMTMSNPPDWTKNVEYFTGI YTFESLI KI I ARGFCL	180
Qy	181	EDFTFLRDPWNLDFTVI TFAYVTEFVDLGNVSALRTFRVLRALKTI SVI PGLKTI VGAL	240
Db	181	EDFTFLRDPWNLDFTVI TFAYVTEFVDLGNVSALRTFRVLRALKTI SVI PGLKTI VGAL	240
Qy	241	I QSVKKLSDVM LTVFCLSVFALI GLQLFMGNLRNKCI QWPPTNASLEEHSI EKNI TVNY	300
Db	241	I QSVKKLSDVM LTVFCLSVFALI GLQLFMGNLRNKCVQWPPTNASLEEHSI EKNVTTDY	300
Qy	301	NGTLI NETVFEFDWKS YI QDSRYHYFLEGFLDALLCGNSSDAGQCPEGYMCVKAGRNP NY	360
Db	301	NGTLVNETVFEFDWKS YI QDSRYHYFLEGFLDALLCGNSSDAGQCPEGYMCVKAGRNP NY	360
Qy	361	GYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYM FFVLVI FLGSFYLI NLI LA	420
Db	361	GYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYM FFVLVI FLGSFYLI NLI LA	420
Qy	421	VVAMAYEEQNQATLEEAEQKEAEFQQMIEQLKKQQEAAQQAATATASEHSREPSAAGRLS	480
Db	421	VVAMAYEEQNQATLEEAEQKEAEFQQMIEQLKKQQEAAQQAATATASEHSREPSAAGRLS	480
Qy	481	DSSSEASKLSSSAKERRNRRKKRKQKEQSGGEEKDEDEFQKSESEDSI RRKGFRFSI EG	540
Db	481	DSSSEASKLSSSAKERRNRRKKRKQKEQSGGEEKDDDEFHKSESEDSI RRKGFRFSI EG	540
Qy	541	NRLTYEKRYSSPHQSLLSI RGSLFSPPRNSRTSLFSFRGRAKDVGSENDFADDEHSTFED	600
Db	541	NRLTYEKRYSSPHQSLLSI RGSLFSPPRNSRTSLFSFRGRAKDVGSENDFADDEHSTFED	600
Qy	601	NESRRDSL FVPRRH GERRNSNL SQT SRSSRML AVFPANGKMHSTVDCNGVSL VGGPSVP	660
Db	601	NESRRDSL FVPRRH GERRNSNL SQT SRSSRML AGLPANGKMHSTVDCNGVSL VGGPSVP	660
Qy	661	TSPVGQLLPEVI I DKPATDDNGTTTEEMRKRRSSSFHVSMDFLEDPSQRQRAMSI ASI L	720
Db	661	TSPVGQLLPEVI I DKPATDDNGTTTEEMRKRRSSSFHVSMDFLEDPSQRQRAMSI ASI L	720
Qy	721	TNTVEELEESRQKCPPCWYKFSNI FLI WDCSPYWLKVKHVNLLVMDPFVDLAI TI CI VL	780
Db	721	TNTVEELEESRQKCPPCWYKFSNI FLI WDCSPYWLKVKHVNLLVMDPFVDLAI TI CI VL	780
Qy	781	NTLFMAMEHYPMTDHFNNVL TVGNL VFTGI FTAEMFLKI I AMDPYYFQEGWNI FDGFI V	840
Db	781	NTLFMAMEHYPMTDHFNNVL TVGNL VFTGI FTAEMFLKI I AMDPYYFQEGWNI FDGFI V	840
Qy	841	TLSLVELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLI KI I GNSVGALGNLTIVLAI I	900
Db	841	TLSLVELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLI KI I GNSVGALGNLTIVLAI I	900
Qy	901	VFI FAVVGMLFGKSYKDCVCKI ASDCQLPRWHMDFFHSFLI VFRVL CGEW ETMNDCM	960
Db	901	VFI FAVVGMLFGKSYKDCVCKI ATDCKLPRWHMDFFHSFLI VFRVL CGEW ETMNDCM	960
Qy	961	EVAGQAMCLTVFMMMWI GNLVVLNLFLALLSSFSADNLAAATDDDNEMNNLQI AVDRMH	1020
Db	961	EVAGQAMCLTVFMMMWI RNLVVLNLFLALLSSFSADNLAAATDDDNEMNNLQI AVDRMH	1020
Qy	1021	KGVAYVKRKI YEFI QQSFIRKQKLI DLEI KPLDDLNNKKDSCMSNHTAEI GKLDYLDKV	1080

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Db 1021 KGAYVKRKI YEFI QQSFRKQKI LDEI KPLDDLNRRKDNTSNHTTEI GKDDCLKDVN 1080
Qy 1081 GTTSGI GTGSSVEKYI | DESDYMSFI NNPSLT TVTVPI AVGESDFENLNTEDFSSESDLEE 1140
Db 1081 GTTSGI GTGSSVEKYI | DESDYMSFI NNPSLT TVTVPI AVGESDFENLNTEDFSSESDLEE 1140
Qy 1141 SKEKLNESSSSSEGSTVDI GAPVEEQPWEPEETLEPEACFTEGCVQRFKCCQI NVEEGR 1200
Db 1141 SKEKLNESSSSSEGSTVDI GAPAEEQPWEPEETLEPEACFTEGCVQRFKCCQI SVEEGR 1200
Qy 1201 GKQWNLRRTCFRI VEHNWFETFI VFM LLSSGALAFEDI YI DQRKTI KTMLEYADKVFT 1260
Db 1201 GKQWNLRRTCFRI VEHNWFETFI VFM LLSSGALAFEDI YI DQRKTI KTMLEYADKVFT 1260
Qy 1261 YI FI LEMLLKWAYGYQTYFTNAWCWDFLI VDVSLSVSLTANALGYSELGAI KSLRTLRA 1320
Db 1261 YI FI LEMLLKWAYGYQTYFTNAWCWDFLI VDVSLSVSLTANALGYSELGAI KSLRTLRA 1320
Qy 1321 LRPLRALSRFEGMRRVNNALLGAI PSI MNVLLVCLI FWI FSI MGVLFAFKFYHCI NTT 1380
Db 1321 LRPLRALSRFEGMRRVNNALLGAI PSI MNVLLVCLI FWI FSI MGVLFAFKFYHCVNTT 1380
Qy 1381 TGDRFDI EDVNNHTDCLKLI ERNETARWKNVKVNFDNVFGYLSLLQATFKGWDI MYA 1440
Db 1381 TGDTFEI TEVNNHSDCLKLI ERNETARWKNVKVNFDNVFGYLSLLQATFKGWDI MYA 1440
Qy 1441 AVDSRNVELQPKYEESLYMYLYFVI FI | FGSSFTLNLFI GVI | DNFNQQKKFGGQDI FM 1500
Db 1441 AVDSRNVELQPKYEESLYMYLYFVI FI | FGSSFTLNLFI GVI | DNFNQQKKFGGQDI FM 1500
Qy 1501 TEEQKYYNAMKKLGSKKPQKPI PRPGNKFQGMWDFVTRQVFDI SIMLI CLNIMTMM 1560
Db 1501 TEEQKYYNAMKKLGSKKPQKPI PRPGNKFQGMWDFVTRQVFDI SIMLI CLNIMTMM 1560
Qy 1561 ETDDQSEYVTTI LSRI NLVFI VLFTGECVLKLI SLRHYYFTI GWN FDFVVI LSI VGMF 1620
Db 1561 ETDDQSDYVTSI LSRI NLVFI VLFTGECVLKLI SLRHYYFTI GWN FDFVVI LSI VGMF 1620
Qy 1621 LAELI EKYFVSPTLFRVI RLARI GRI LRLI KGAKGI RTLLFALMMSLPALFNI GLLLFLV 1680
Db 1621 LAELI EKYFVSPTLFRVI RLARI GRI LRLI KGAKGI RTLLFALMMSLPALFNI GLLLFLV 1680
Qy 1681 MFI YAI FGMSNFAYVKREVGIDDMFNFETFGNSM CLFQI TTSGWDGLAPI LNSKPPD 1740
Db 1681 MFI YAI FGMSNFAYVKREVGIDDMFNFETFGNSM CLFQI TTSGWDGLAPI LNSKPPD 1740
Qy 1741 CDPNKVNPGSSVKGDCGNPSVG IFFFVSYI | SFL VVNM YI AVI LENFSVATEESAEP 1800
Db 1741 CDPNKVNPGSSVKGDCGNPSVG IFFFVSYI | SFL VVNM YI AVI LENFSVATEESAEP 1800
Qy 1801 SEDDFEMFYEVWKEFDPDATQFMEFEKLSQFAAAL EPPLNL PQPNKLQLI AMDLPMMSGD 1860
Db 1801 SEDDFEMFYEVWKEFDPDATQFMEFEKLSQFAAAL EPPLNL PQPNKLQLI AMDLPMMSGD 1860
Qy 1861 RI HCLDI LFAFTKRLGESGEMDALRI QMEERFMASNPSKVSYQPI TTTLKRKQEEVSAV 1920
Db 1861 RI HCLDI LFAFTKRLGESGEMDALRI QMEERFMASNPSKVSYQPI TTTLKRKQEEVSAV 1920
Qy 1921 || QRAYRRHLLKRTVKQASFTYNKNKI KGGANLLI KEDM | DRI NENSI TEKDLTMSTA 1980
Db 1921 || QRAYRRHLLKRTVKQASFTYNKNKLKGGANLLVKEDM | DRI NENSI TEKDLTMSTA 1980
Qy 1981 ACPPSYDRVTKPI VEKHEQEGKDEKAKGK 2009

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Db 1981 ACPPSYDRVTKPI VEKHEQEGKDEKAKGK 2009

Search completed: June 5, 2008, 12:26:53
Job time : 2 secs